

1 / 143

SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

THE UNIVERSITY OF TOKYO

<120> METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCER

<130> ONC-A0401P

<150> US 60/555,789

<151> 2004-03-23

<160> 127

<170> PatentIn version 3.3

<210> 1

<211> 4908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (141)..(3311)

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atTTTTTggc ggggaccgtc atg gcg tcg cag cca aat tcg tct gcg aag aag 173

Met Ala Ser Gln Pro Asn Ser Ser Ala Lys Lys

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aaa gag gag aag ggg aag aac atc cag gtg gtg gtg aga tgc aga cca 221

Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro

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Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys

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gat cct gta cga aaa gaa gtt agt gta cga act gga gga ttg gct gac 317

Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp

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aag agc tca agg aaa aca tac act ttt gat atg gtg ttt gga gca tct 365

Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser

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act aaa cag att gat gtt tac cga agt gtt gtt tgt cca att ctg gat 413

3 / 1 4 3

Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp

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gaa gtt att atg ggc tat aat tgc act atc ttt gcg tat ggc caa act 461

Glu Val Ile Met Gly Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr

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ggc act gga aaa act ttt aca atg gaa ggt gaa agg tca cct aat gaa 509

Gly Thr Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu

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gag tat acc tgg gaa gag gat ccc ttg gct ggt ata att cca cgt acc 557

Glu Tyr Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr

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ctt cat caa att ttt gag aaa ctt act gat aat ggt act gaa ttt tca 605

Leu His Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser

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gtc aaa gtg tct ctg ttg gag atc tat aat gaa gag ctt ttt gat ctt 653

Val Lys Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu

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ctt aat cca tca tct gat gtt tct gag aga cta cag atg ttt gat gat 701

Leu Asn Pro Ser Ser Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp

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ccc cgt aac aag aga gga gtg ata att aaa ggt tta gaa gaa att aca 749
Pro Arg Asn Lys Arg Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr
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gta cac aac aag gat gaa gtc tat caa att tta gaa aag ggg gca gca 797
Val His Asn Lys Asp Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala Ala
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aaa agg aca act gca gct act ctg atg aat gca tac tct agt cgt tcc 845
Lys Arg Thr Thr Ala Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser
220 225 230 235

cac tca gtt ttc tct gtt aca ata cat atg aaa gaa act acg att gat 893
His Ser Val Phe Ser Val Thr Ile His Met Lys Glu Thr Thr Ile Asp
240 245 250

gga gaa gag ctt gtt aaa atc gga aag ttg aac ttg gtt gat ctt gca 941
Gly Glu Glu Leu Val Lys Ile Gly Lys Leu Asn Leu Val Asp Leu Ala
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Gly Ser Glu Asn Ile Gly Arg Ser Gly Ala Val Asp Lys Arg Ala Arg
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gaa gct gga aat ata aat caa tcc ctg ttg act ttg gga agg gtc att 1037

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Glu Ala Gly Asn Ile Asn Gln Ser Leu Leu Thr Leu Gly Arg Val Ile

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act gcc ctt gta gaa aga aca cct cat gtt cct tat cga gaa tet aaa 1085

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cta act aga atc etc cag gat tct ctt gga ggg cgt aca aga aca tct 1133

Leu Thr Arg Ile Leu Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser

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ata att gca aca att tct cct gca tct etc aat ctt gag gaa act ctg 1181

Ile Ile Ala Thr Ile Ser Pro Ala Ser Leu Asn Leu Glu Glu Thr Leu

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Ser Thr Leu Glu Tyr Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro

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gaa gtg aat cag aaa etc acc aaa aaa gct ctt att aag gag tat acg 1277

Glu Val Asn Gln Lys Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr

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gag gag ata gaa cgt tta aaa cga gat ctt gct gca gcc cgt gag aaa 1325

Glu Glu Ile Glu Arg Leu Lys Arg Asp Leu Ala Ala Ala Arg Glu Lys

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Asn Gly Val Tyr Ile Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys	
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Leu Thr Val Gln Glu Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly	
415 420 425	
gct gtt gag gag gag ctg aat agg gtt aca gag ttg ttt atg gat aat	1469
Ala Val Glu Glu Glu Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn	
430 435 440	
aaa aat gaa ctt gac cag tgt aaa tct gac ctg caa aat aaa aca caa	1517
Lys Asn Glu Leu Asp Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln	
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Glu Leu Glu Thr Thr Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu	
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Val Lys Glu Glu Tyr Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys	
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Lys Asp Val Ser Gly Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val

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caa aag gcc atg cta gaa gta cat aag acc tta ttt ggt aat ctg ctg 1853

Gln Lys Ala Met Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu

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Ser Ser Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly

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Ser Leu Thr Ser Ile Pro Glu Asn Val Ser Thr His Val Ser Gln Ile

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ctg gaa atg att tta tcc cca act gtg gtg tct ata ctg aaa atc aat 2093

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Asn Asn Leu His Glu Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu

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Ser Gln Lys Gln Cys Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys

700 705 710 715

cag acc cat tcc cag gaa ctt tgc aag tta atg aat ctt tgg aca gag 2333

Gln Thr His Ser Gln Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu

720 725 730

aga ttc tgt gct ttg gag gaa aag tgt gaa aat ata cag aaa cca ctt 2381

Arg Phe Cys Ala Leu Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu

735 740 745

agt agt gtc cag gaa aat ata cag cag aaa tct aag gat ata gtc aac 2429

Ser Ser Val Gln Glu Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn

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Lys Met Thr Phe His Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe

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tca cag gaa ctc aga aat ttt aac caa gaa ggt aca aaa ttg gtt gaa 2525

Ser Gln Glu Leu Arg Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu

780 785 790 795

gaa tct gtg aaa cac tct gat aaa ctc aat ggc aac ctg gaa aaa ata 2573

Glu Ser Val Lys His Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile

800 805 810

10/143

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Ser Gln Glu Thr Glu Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val	
815 820 825	
tat ttt tot gaa cag tgg gta tot tcc tta aat gaa agg gaa cag gaa	2669
Tyr Phe Ser Glu Gln Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu	
830 835 840	
ctt cac aac tta ttg gag gtt gta agc caa tgt tgt gag gct tca agt	2717
Leu His Asn Leu Leu Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser	
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Ser Asp Ile Thr Glu Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys	
860 865 870 875	
cag cat aac att ttt ctt gat cag atg act att gat gaa gat aaa ttg	2813
Gln His Asn Ile Phe Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu	
880 885 890	
ata gca caa aat cta gaa ctt aat gaa acc ata aaa att ggt ttg act	2861
Ile Ala Gln Asn Leu Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr	
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ggc acg aca cca cag agg aaa agt tat tta tac cca tca aca ctg gta 2957

Gly Thr Thr Pro Gln Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val

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aga act gaa cca cgt gaa cat ctc ctt gat cag ctg aaa agg aaa cag 3005

Arg Thr Glu Pro Arg Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln

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cct gag ctg tta atg atg cta aac tgt tca gaa aac aac aaa gaa gag 3053

Pro Glu Leu Leu Met Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu

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aca att ccg gat gtg gat gta gaa gag gca gtt ctg ggg cag tat act 3101

Thr Ile Pro Asp Val Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr

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Glu Glu Pro Leu Ser Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys

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1 5 / 1 4 3

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20

25

30

Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg Lys

35

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45

Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys

50

55

60

Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp

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70

75

80

Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly

85

90

95

Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr

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Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu

1 6 / 1 4 3

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Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe

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135

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Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu

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160

Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser

165

170

175

Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg

180

185

190

Glu Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His Asn Lys Asp

195

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205

Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala Ala Lys Arg Thr Thr Ala

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220

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Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser Val Phe Ser
225 230 235 240

Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu Glu Leu Val
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Lys Ile Gly Lys Leu Asn Leu Val Asp Leu Ala Gly Ser Glu Asn Ile
260 265 270

Gly Arg Ser Gly Ala Val Asp Lys Arg Ala Arg Glu Ala Gly Asn Ile
275 280 285

Asn Gln Ser Leu Leu Thr Leu Gly Arg Val Ile Thr Ala Leu Val Glu
290 295 300

Arg Thr Pro His Val Pro Tyr Arg Glu Ser Lys Leu Thr Arg Ile Leu
305 310 315 320

Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser Ile Ile Ala Thr Ile

1 8 / 1 4 3

325

330

335

Ser Pro Ala Ser Leu Asn Leu Glu Glu Thr Leu Ser Thr Leu Glu Tyr

340

345

350

Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro Glu Val Asn Gln Lys

355

360

365

Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr Glu Glu Ile Glu Arg

370

375

380

Leu Lys Arg Asp Leu Ala Ala Ala Arg Glu Lys Asn Gly Val Tyr Ile

385

390

395

400

Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys Leu Thr Val Gln Glu

405

410

415

Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly Ala Val Glu Glu Glu

420

425

430

1 9 / 1 4 3

Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn Lys Asn Glu Leu Asp

435

440

445

Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln Glu Leu Glu Thr Thr

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460

Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu Val Lys Glu Glu Tyr

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Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys Leu His Asp Ala Ala

485

490

495

Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr Lys Asp Val Ser Gly

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505

510

Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val Asp Gln His Asn Ala

515

520

525

Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn Ser Leu Phe Asn Asn

20 / 143

530

535

540

Met Glu Glu Leu Ile Lys Asp Gly Ser Ser Lys Gln Lys Ala Met Leu

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550

555

560

Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu Ser Ser Ser Val Ser

565

570

575

Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly Ser Leu Thr Ser Ile

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585

590

Pro Glu Asn Val Ser Thr His Val Ser Gln Ile Phe Asn Met Ile Leu

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600

605

Lys Glu Gln Ser Leu Ala Ala Glu Ser Lys Thr Val Leu Gln Glu Leu

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615

620

Ile Asn Val Leu Lys Thr Asp Leu Leu Ser Ser Leu Glu Met Ile Leu

625

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635

640

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Ser Pro Thr Val Val Ser Ile Leu Lys Ile Asn Ser Gln Leu Lys His

645

650

655

Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys Ile Glu Asp Gln Lys

660

665

670

Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys Asn Asn Leu His Glu

675

680

685

Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu Ser Gln Lys Gln Cys

690

695

700

Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys Gln Thr His Ser Gln

705

710

715

720

Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu Arg Phe Cys Ala Leu

725

730

735

Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu Ser Ser Val Gln Glu

2 2 / 1 4 3

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745

750

Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn Lys Met Thr Phe His

755

760

765

Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe Ser Gln Glu Leu Arg

770

775

780

Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu Glu Ser Val Lys His

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Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile Ser Gln Glu Thr Glu

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810

815

Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val Tyr Phe Ser Glu Gln

820

825

830

Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu His Asn Leu Leu

835

840

845

2 3 / 1 4 3

Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser Asp Ile Thr Glu

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860

Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys Gln His Asn Ile Phe

865

870

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880

Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile Ala Gln Asn Leu

885

890

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Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys Phe

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905

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Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro Gln

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920

925

Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg Thr Glu Pro Arg

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935

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Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro Glu Leu Leu Met

2 4 / 1 4 3

945

950

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Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp Val

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970

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Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr Glu Glu Pro Leu Ser

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Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys Ser Ser Ile Gly Gly

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1005

Val Pro Phe Phe Gln His Lys Lys Ser His Gly Lys Asp Lys Glu

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Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp

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gag ctg ctg cag ctc ttc ccc gcg ccg ctg ctg gcg ggc gtc aca gcc 144

Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala

2 6 / 1 4 3

35

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45

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 Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
 50 55 60

atg ctg gtg gtg tcg cgc ttc cgc gag ctg cgc acc acc acc aac ctc 240
 Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
 65 70 75 80

tac ctg tcc agc atg gcc ttc tcc gat ctg ctc atc ttc ctc tgc atg 288
 Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
 85 90 95

ccc ctg gac ctc gtt cgc ctc tgg cag tac cgg ccc tgg aac ttc ggc 336
 Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly
 100 105 110

gac ctc ctc tgc aaa ctc ttc caa ttc gtc agt gag agc tgc acc tac 384
 Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
 115 120 125

gcc acg gtg ctc acc atc aca gcg ctg agc gtc gag cgc tac ttc gcc 432
 Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
 130 135 140

27/143

atc tgc ttc cca ctc cgg gcc aag gtg gtg gtc acc aag ggg cgg gtg 480
Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
145 150 155 160

aag ctg gtc atc ttc gtc atc tgg gcc gtg gcc ttc tgc agc gcc ggg 528
Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
165 170 175

ccc atc ttc gtg cta gtc ggg gtg gag cac gag aac ggc acc gac cct 576
Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
180 185 190

tgg gac acc aac gag tgc cgc ccc acc gag ttt gcg gtg cgc tct gga 624
Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
195 200 205

ctg ctc acg gtc atg gtg tgg gtg tcc agc atc ttc ttc ttc ctt cct 672
Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
210 215 220

gtc ttc tgt ctc acg gtc ctc tac agt ctc atc ggc agg aag ctg tgg 720
Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp
225 230 235 240

cgg agg agg cgc ggc gat gct gtc gtg ggt gcc tcg ctc agg gac cag 768
Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln

2 8 / 1 4 3

245

250

255

aac cac aag caa acc gtg aaa atg ctg ggt ggg tct cag cgc gcg ctc 816

Asn His Lys Gln Thr Val Lys Met Leu Gly Gly Ser Gln Arg Ala Leu

260

265

270

agg ctt tet ctc gcg ggt cct atc ctc tcc ctg tgc ctt ctc cct tct 864

Arg Leu Ser Leu Ala Gly Pro Ile Leu Ser Leu Cys Leu Leu Pro Ser

275

280

285

ctc tga

870

Leu

<210> 4

<211> 289

<212> PRT

<213> Homo sapiens

<400> 4

Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu

1

5

10

15

29/143

Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp

20

25

30

Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala

35

40

45

Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr

50

55

60

Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu

65

70

75

80

Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met

85

90

95

Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly

100

105

110

Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr

115

120

125

3 0 / 1 4 3

Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
130 135 140

Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
145 150 155 160

Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
165 170 175

Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
180 185 190

Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
195 200 205

Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
210 215 220

3 1 / 1 4 3

Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp

225

230

235

240

Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln

245

250

255

Asn His Lys Gln Thr Val Lys Met Leu Gly Gly Ser Gln Arg Ala Leu

260

265

270

Arg Leu Ser Leu Ala Gly Pro Ile Leu Ser Leu Cys Leu Leu Pro Ser

275

280

285

Leu

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<211> 4131

<212> DNA

<213> Homo sapiens

3 2 / 1 4 3

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cccgaggaac cacgggttct ggagctagga gccggaagct gggagtcgg aggagagcgg	180
agcccgagac ccggagcccg gggcggcgcg tctgggtctg gcgttcccg actggacggc	240
gcgcccgtcg gtcttcgcca cgcgccctcc cctgggctcg cgttcacgg tcccgcctg	300
agacgcgccc actcctgccc gaacttcag ccccgagggc gccggacaga gccgcggact	360
ccagcgccca cc atg cgc etc aac agc tcc gcg ccg gga acc ccg ggc acg	411
Met Arg Leu Asn Ser Ser Ala Pro Gly Thr Pro Gly Thr	
1 5 10	
ccg gcc gcc gac ccc ttc cag cgg gcg cag gcc gga ctg gag gag gcg	459
Pro Ala Ala Asp Pro Phe Gln Arg Ala Gln Ala Gly Leu Glu Glu Ala	
15 20 25	
ctg ctg gcc ccg ggc ttc ggc aac gct tcg ggc aac gcg tcg gag cgc	507

3 3 / 1 4 3

Leu Leu Ala Pro Gly Phe Gly Asn Ala Ser Gly Asn Ala Ser Glu Arg .

30

35

40

45

gtc ctg gcg gca ccc agc agc gag ctg gac gtg aac acc gac atc tac 555

Val Leu Ala Ala Pro Ser Ser Glu Leu Asp Val Asn Thr Asp Ile Tyr

50

55

60

tcc aaa gtg ctg gtg acc gcc gtg tac ctg gcg ctc ttc gtg gtg ggc 603

Ser Lys Val Leu Val Thr Ala Val Tyr Leu Ala Leu Phe Val Val Gly

65

70

75

acg gtg ggc aac acg gtg acg gcg ttc acg ctg gcg cgg aag aag tgc 651

Thr Val Gly Asn Thr Val Thr Ala Phe Thr Leu Ala Arg Lys Lys Ser

80

85

90

ctg cag agc ctg cag agc acg gtg cat tac cac ctg ggc agc ctg gcg 699

Leu Gln Ser Leu Gln Ser Thr Val His Tyr His Leu Gly Ser Leu Ala

95

100

105

ctg tcc gac ctg ctc acc ctg ctg ctg gcc atg ccc gtg gag ctg tac 747

Leu Ser Asp Leu Leu Thr Leu Leu Leu Ala Met Pro Val Glu Leu Tyr

110

115

120

125

aac ttc atc tgg gtg cac cac ccc tgg gcc ttc ggc gac gcc ggc tgc 795

Asn Phe Ile Trp Val His His Pro Trp Ala Phe Gly Asp Ala Gly Cys

130

135

140

3 4 / 1 4 3

cgc ggc tac tac ttc ctg cgc gac gcc tgc acc tac gcc acg gcc ctc	843
Arg Gly Tyr Tyr Phe Leu Arg Asp Ala Cys Thr Tyr Ala Thr Ala Leu	
145 150 155	
aac gtg gcc agc ctg agt gtg gag cgc tac ctg gcc atc tgc cac ccc	891
Asn Val Ala Ser Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys His Pro	
160 165 170	
ttc aag gcc aag acc ctc atg tcc cga agc cgc acc aag aag ttc atc	939
Phe Lys Ala Lys Thr Leu Met Ser Arg Ser Arg Thr Lys Lys Phe Ile	
175 180 185	
agc gcc atc tgg ctc gcc tcg gcc ctg ctg acg gtg cct atg ctg ttc	987
Ser Ala Ile Trp Leu Ala Ser Ala Leu Leu Thr Val Pro Met Leu Phe	
190 195 200 205	
acc atg ggc gag cag aac cgc agc gcc gac ggc cag cac gcc ggc ggc	1035
Thr Met Gly Glu Gln Asn Arg Ser Ala Asp Gly Gln His Ala Gly Gly	
210 215 220	
ctg gtg tgc acc ccc acc atc cac act gcc acc gtc aag gtc gtc ata	1083
Leu Val Cys Thr Pro Thr Ile His Thr Ala Thr Val Lys Val Val Ile	
225 230 235	
cag gtc aac acc ttc atg tcc ttc ata ttc ccc atg gtg gtc atc tcg	1131

3 5 / 1 4 3

Gln Val Asn Thr Phe Met Ser Phe Ile Phe Pro Met Val Val Ile Ser .

240

245

250

gtc ctg aac acc atc atc gcc aac aag ctg acc gtc atg gta cgc cag 1179

Val Leu Asn Thr Ile Ile Ala Asn Lys Leu Thr Val Met Val Arg Gln

255

260

265

gcg gcc gag cag ggc caa gtg tgc acg gtc ggg ggc gag cac agc aca 1227

Ala Ala Glu Gln Gly Gln Val Cys Thr Val Gly Gly Glu His Ser Thr

270

275

280

285

ttc agc atg gcc atc gag cct ggc agg gtc cag gcc ctg cgg cac gcc 1275

Phe Ser Met Ala Ile Glu Pro Gly Arg Val Gln Ala Leu Arg His Gly

290

295

300

gtg cgc gtc cta cgt gca gtg gtc atc gcc ttt gtg gtc tgc tgg ctg 1323

Val Arg Val Leu Arg Ala Val Val Ile Ala Phe Val Val Cys Trp Leu

305

310

315

ccc tac cac gtg cgg cgc ctc atg ttc tgc tac atc tcg gat gag cag 1371

Pro Tyr His Val Arg Arg Leu Met Phe Cys Tyr Ile Ser Asp Glu Gln

320

325

330

tgg act ccg ttc ctc tat gac ttc tac cac tac ttc tac atg gtg acc 1419

Trp Thr Pro Phe Leu Tyr Asp Phe Tyr His Tyr Phe Tyr Met Val Thr

335

340

345

3 6 / 1 4 3

aac gca ctc ttc tac gtc agc tcc acc atc aac ccc atc ctg tac aac 1467
Asn Ala Leu Phe Tyr Val Ser Ser Thr Ile Asn Pro Ile Leu Tyr Asn
350 355 360 365

ctc gtc tct gcc aac ttc cgc cac atc ttc ctg gcc aca ctg gcc tgc 1515
Leu Val Ser Ala Asn Phe Arg His Ile Phe Leu Ala Thr Leu Ala Cys
370 375 380

ctc tgc ccg gtg tgg cgg cgc agg agg aag agg cca gcc ttc tcg agg 1563
Leu Cys Pro Val Trp Arg Arg Arg Arg Lys Arg Pro Ala Phe Ser Arg
385 390 395

aag gcc gac agc gtg tcc agc aac cac acc ctc tcc agc aat gcc acc 1611
Lys Ala Asp Ser Val Ser Ser Asn His Thr Leu Ser Ser Asn Ala Thr
400 405 410

cgc gag acg ctg tac tag gctgtgcgcc ccggaacgtg tccaggagga 1659
Arg Glu Thr Leu Tyr
415

gcctggccat gggtccttgc ccccgacaga cagagcagcc cccacccggg agccttcatg 1719

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3 7 / 1 4 3

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gcctctaaca aggagaaatt agtgtcggcg aaaaggcagt ttctttgtt ctgagactaa 1959

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3 8 / 1 4 3

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catttgtcac cttctggcgg cggcagocct ggccccggcc tccaagcagt tgaaaaagct 2799

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caacccagg gaaacagggc cagcacagag gggccttct cccccacaga gtcccatga 3399

3 9 / 1 4 3

catagtctgc tctgggcgga agagctttgc tgccagccag ggatgtccag aggtcgggtgc 3459

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tgatgtggcc ccggaagctg gccctgcgtg coatgagtgc gtcggtcatg gagtccggag 3999

ccctgagcc ggccccctggt gaaggcacag ccttcacagc taaaagccc acccccactc 4059

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40/143

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<213> Homo sapiens

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Asp Pro Phe Gln Arg Ala Gln Ala Gly Leu Glu Glu Ala Leu Leu Ala
20 25 30

Pro Gly Phe Gly Asn Ala Ser Gly Asn Ala Ser Glu Arg Val Leu Ala
35 40 45

Ala Pro Ser Ser Glu Leu Asp Val Asn Thr Asp Ile Tyr Ser Lys Val
50 55 60

Leu Val Thr Ala Val Tyr Leu Ala Leu Phe Val Val Gly Thr Val Gly

4 1 / 1 4 3

65 70 75 80

Asn Thr Val Thr Ala Phe Thr Leu Ala Arg Lys Lys Ser Leu Gln Ser

85 90 95

Leu Gln Ser Thr Val His Tyr His Leu Gly Ser Leu Ala Leu Ser Asp

100 105 110

Leu Leu Thr Leu Leu Leu Ala Met Pro Val Glu Leu Tyr Asn Phe Ile

115 120 125

Trp Val His His Pro Trp Ala Phe Gly Asp Ala Gly Cys Arg Gly Tyr

130 135 140

Tyr Phe Leu Arg Asp Ala Cys Thr Tyr Ala Thr Ala Leu Asn Val Ala

145 150 155 160

Ser Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys His Pro Phe Lys Ala

165 170 175

4 2 / 1 4 3

Lys Thr Leu Met Ser Arg Ser Arg Thr Lys Lys Phe Ile Ser Ala Ile
180 185 190

Trp Leu Ala Ser Ala Leu Leu Thr Val Pro Met Leu Phe Thr Met Gly
195 200 205

Glu Gln Asn Arg Ser Ala Asp Gly Gln His Ala Gly Gly Leu Val Cys
210 215 220

Thr Pro Thr Ile His Thr Ala Thr Val Lys Val Val Ile Gln Val Asn
225 230 235 240

Thr Phe Met Ser Phe Ile Phe Pro Met Val Val Ile Ser Val Leu Asn
245 250 255

Thr Ile Ile Ala Asn Lys Leu Thr Val Met Val Arg Gln Ala Ala Glu
260 265 270

Gln Gly Gln Val Cys Thr Val Gly Gly Glu His Ser Thr Phe Ser Met

4 3 / 1 4 3

275

280

285

Ala Ile Glu Pro Gly Arg Val Gln Ala Leu Arg His Gly Val Arg Val

290

295

300

Leu Arg Ala Val Val Ile Ala Phe Val Val Cys Trp Leu Pro Tyr His

305

310

315

320

Val Arg Arg Leu Met Phe Cys Tyr Ile Ser Asp Glu Gln Trp Thr Pro

325

330

335

Phe Leu Tyr Asp Phe Tyr His Tyr Phe Tyr Met Val Thr Asn Ala Leu

340

345

350

Phe Tyr Val Ser Ser Thr Ile Asn Pro Ile Leu Tyr Asn Leu Val Ser

355

360

365

Ala Asn Phe Arg His Ile Phe Leu Ala Thr Leu Ala Cys Leu Cys Pro

370

375

380

4 4 / 1 4 3

Val Trp Arg Arg Arg Arg Lys Arg Pro Ala Phe Ser Arg Lys Ala Asp
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Ser Val Ser Ser Asn His Thr Leu Ser Ser Asn Ala Thr Arg Glu Thr
 405 410 415

Leu Tyr

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<212> DNA

<213> Artificial

<220>

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23

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<400> 10

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22

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actgagaaca ttgacaacac agg

23

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<211> 22

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aagagggaca gggacaagta gt

22

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<211> 21

<212> DNA

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48/143

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21

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<212> DNA

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<210> 16

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<400> 16

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tgatacagag acatgaagtg agca

24

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<212> DNA

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<210> 18

<211> 20

<212> DNA

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<220>

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<400> 18

gaatcccaga agtctgaaca

20

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<220>

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<400> 19

acggtcctct acagtctca

19

<210> 20

<211> 18

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<223> An artificially synthesized primer sequence for RT-PCR

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18

<210> 21

5 1 / 1 4 3

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

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23

<210> 22

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23

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5 2 / 1 4 3

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<223> An artificially synthesized primer sequence for RT-PCR

<400> 23

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21

<210> 25

<211> 22

<212> DNA

<213> Artificial

5 3 / 1 4 3

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<223> An artificially synthesized primer sequence for RT-PCR

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22

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<212> DNA

<213> Artificial

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<223> An artificially synthesized primer sequence for RT-PCR

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24

<210> 27

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<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

5 4 / 1 4 3

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gaggtgatag cattgctttc g

21

<210> 28

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 28

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21

<210> 29

<211> 19

<212> DNA

<213> Artificial

<220>

<223> A target sequence for siRNA

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<213> Artificial

<220>

<223> A target sequence for siRNA

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19

<210> 31

<211> 19

<212> DNA

<213> Artificial

<220>

<223> A target sequence for siRNA

<400> 31

gcgcgctttg taggattcg

19

5 6 / 1 4 3

<210> 32

<211> 19

<212> DNA

<213> Artificial

<220>

<223> A target sequence for siRNA

<400> 32

gttagtgtac gaactggag

19

<210> 33

<211> 19

<212> DNA

<213> Artificial

<220>

<223> A target sequence for siRNA

<400> 33

gtgtctctgt tggagatct

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<210> 34

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<211> 19

<212> DNA

<213> Artificial

<220>

<223> A target sequence for siRNA

<400> 34

gaaggcagtt gaccaacac

19

<210> 35

<211> 19

<212> DNA

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<220>

<223> A target sequence for siRNA

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<223> A target sequence for siRNA

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ggctgctcata caggtcaac

19

<210> 38

<211> 32

<212> DNA

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32

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<211> 40

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<223> An artificially synthesized primer sequence for RT-PCR

<400> 39

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<210> 40

<211> 32

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

6 0 / 1 4 3

<400> 40

ggaattccat gtggaacgcg acgcccagcg aa

32

<210> 41

<211> 36

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 41

cgcggatccg cggagagaag ggagaaggca cagggga

36

<210> 42

<211> 36

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 42

6 1 / 1 4 3

ggaattccat gcgcctcaac agctccgcgc cgggaa

36

<210> 43

<211> 39

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 43

cgcgatccg cggtagacgc tctcgcggt ggcattgct

39

<210> 44

<211> 22

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of H1RNA gene
promoter region

<400> 44

tggtagccaa gtgcaggta ta

22

6 2 / 1 4 3

<210> 45

<211> 22

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of H1RNA gene
promoter region

<400> 45

ccaaagggtt tctgcagttt ca

22

<210> 46

<211> 30

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of pcDNA3.1
H1RNA gene fragment

<400> 46

tgcggatcca gagcagattg tactgagagt

30

6 3 / 1 4 3

<210> 47

<211> 29

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of pcDNA3.1
H1RNA gene fragment

<400> 47

ctctatctcg agtgaggcgg aaagaacca

29

<210> 48

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of the
ligated DNA

<400> 48

tttaagcttg aagaccattt ttggaaaaaa aaaaaaaaaa aaaaaaac

47

6 4 / 1 4 3

<210> 49

<211> 34

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of the
ligated DNA

<400> 49

tttaagcttg aagacatggg aaagagtgg ctca

34

<210> 50

<211> 5085

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized vector sequence

<400> 50

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60

6 5 / 1 4 3

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ggagctgaag ggaagggggt cacagtaggt ggcatcggtt ctttctgact gcccgcccc 180

cgcatgccgt ccgcgatat tgagctccga acctctcgcc ctgccgccg cggtgctccg 240

tcgccgccg gccgccatgg aattcgaacg ctgacgtcat caaccgctc caaggaaatcg 300

cgggccagtg gtactaggc gggaacaccc agcgcgctg cgccctggca ggaagatggc 360

tgtgagggac aggggagtg cgccctgcaa tatttgcatg tcgctatgtg ttctgggaaa 420

tcaccataaa cgtgaaatgt ctttgattt gggaatttta taagtctgt atgagaccac 480

tctttccctt ttgggaaaa aaaaaaaaaa aaaaaaacg aaaccgggcc gggcgcggtg 540

gttcacgctt ataattccag cactttggga ggccgaggcg ggcggatcac aaggtcagga 600

ggtcgagacc atccaggcta acacggtgaa accccccccc atctctacta aaaaaaaaaa 660

atacaaaaaa ttagccatta gccggcgctg gtggcgggcg cctataatcc cagctacttg 720

ggaggctgaa gcagaatggc gtgaaccggg gaggcggacg ttgcagtgag ccgagatgcg 780

gccgactgca ttccagcctg ggcgacagag cgagtctcaa aaaaaaaccc gagtggaatg 840

6 6 / 1 4 3

tgaaaagctc cgtgaaactg cagaaaccca agccgaattc tgcagatata catcacactg 900

gcggccgctc gagtgaggcg gaaagaacca gctggggctc taggggggtat cccacacgcg 960

cctgtagcgg cgcattaagc gcggcgggtg tgggtggttac gcgcagcgtg accgctacac 1020

ttgccagcgc cctagcgcgc gctcccttcg cttctctccc ttcccttctc gccacgttcg 1080

ccggttttcc ccgtcaagct ctaaatcggg ggctcccttt aggggttcga tttagtgtt 1140

tacggcacct cgaccccaaa aaacttgatt agggatgatg ttcacgtagt gggccatcgc 1200

cctgatagac ggtttttcgc cctttgacgt tggagtccac gttctttaat agtggactct 1260

tgttccaaac tggaacaaca ctcaacccta tctcgggtcta ttcttttgat ttataaggga 1320

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cagaagtatg caaagcatgc atctcaatta gtcagcaacc aggtgtggaa agtccccagg 1500

ctccccagca ggcagaagta tgcaaagcat gcattctaat tagtcagcaa ccatagtccc 1560

gccctaaact ccgcccatcc cgcccctaac tccgccagat tccgccatt ctccgcccac 1620

6 7 / 1 4 3

tggtgacta atttttttta tttatgcaga ggccgaggcc gcctctgcct ctgagctatt 1680

ccagaagtag tgaggaggct tttttggagg cctaggcttt tgcaaaaagc tcccgggagc 1740

ttgtatatcc attttcggat ctgatcaaga gacaggatga ggatcgtttc gcatgattga 1800

acaagatgga ttgcacgcag gttctccggc cgcttgggtg gagaggctat tcggctatga 1860

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ggggctcgcg ccagccgaac tgttcgccag gctcaaggcg cgcatgcccc acggcgagga 2340

tctcgtcgtg acccatggcg atgcctgctt gccgaatc atggtggaaa atggccgctt 2400

68 / 143

ttctggattc atcgactgtg gccggctggg tgtggcggac cgctatcagg acatagcggt 2460

ggctaccogt gatattgctg aagagcttgg cggcgaatgg gctgaccgct tctctgtgct 2520

ttacggtatc gccgctcccg attcgcagcg catcgccctc tatcgccctc ttgacgagtt 2580

cttctgagcg ggactctggg gttcgaaatg accgaccaag cgacgccccaa cctgccatca 2640

cgagatttcg attccaccgc cgccttctat gaaaggttgg gcttcggaat cgttttcogg 2700

gacgcgggct ggatgatcct ccagcgcggg gatctcatgc tggagttctt cggccacccc 2760

aacttgttta ttgcagctta taatggttac aaataaagca atagcatcac aaatttcaca 2820

aataaagcat ttttttact gcattctagt tgtggtttgt ccaaactcat caatgtatct 2880

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tttctgtgt gaaattgtta tccgctcaca attccacaca acatacgagc cggaagcata 3000

aagtgtaaag cctgggggtgc ctaatgagt agctaactca cattaattgc gttgcgtca 3060

ctgcccgctt tccagtcggg aaacctgtgc tgccagctgc attaatgaat cgccaacgc 3120

gcggggagag gcggtttgcg tattgggcgc tcttcgctt cctcgtcac tgactcgtg 3180

6 9 / 1 4 3

cgctcggtcg ttcggtgcg gcgagcggt tcaagtcact caaaggcgg taaacaggtta 3240

tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca gcaaaggcc 3300

aggaaccgta aaaaggccgc gttgctggcg tttttcata ggctccgcc cctgacgag 3360

catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact ataaagatac 3420

caggcggttc cccctggaag ctccctcgtg cgctctcctg ttccgacct gccgcttacc 3480

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tccggcaaac aaaccaccgc tggtagcgtt tttttgttt gcaagcagca gattacgcg 3900

agaaaaaag gatctcaaga agatccttg atcttttcta cggggtctga cgctcagtg 3960

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aacgaaaact cacgttaagg gattttggtc atgagattat caaaaaggat cttcacctag 4020

atccttttaa attaaaaatg aagtttttaa tcaatctaaa gtatatatga gtaaacctgg 4080

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cggagttgct cttgcccgc gtcaatacgg gataatacgg cgccacatag cagaacttta 4740

7 1 / 1 4 3

aaagtgtca tcattgaaa acgtttctcg gggcgaaaac tctcaaggat cttaccgctg 4800
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<210> 51

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
 construction of siRNA expression vector

<400> 51

tcccgtagt gtacgaactg gagttcaaga gactccagtt cgtacactaa c

51

7 2 / 1 4 3

<210> 52

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 52

aaaagttagt gtacgaactg gagtctcttg aactccagtt cgtacactaa c

51

<210> 53

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for hairpin
siRNA

<400> 53

gttagtgtac gaactggagt tcaagagact ccagttcgta cactaac

47

7 3 / 1 4 3

<210> 54

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 54

tcccggtgtct ctgttgaga tctttcaaga gaagatctcc aacagagaca c

51

<210> 55

<211> 51

<212> DNA

<213> Artificial

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construction of siRNA expression vector

<400> 55

aaaagtgtct ctgttgaga tcttctcttg aaagatctcc aacagagaca c

51

7 4 / 1 4 3

<210> 56

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for hairpin
siRNA

<400> 56

gtgtctctgt tggagatctt tcaagagaag atctccaaca gagacac

47

<210> 57

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 57

tcccgaaggc agttgaccaa cacttcaaga gagtgttggt caactgcctt c

51

7 5 / 1 4 3

<210> 58

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 58

aaaagaaggc agtgaccaa cactctcttg aagtgttggt caactgcctt c

51

<210> 59

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for hairpin
siRNA

<400> 59

gaaggcagtt gaccaacact tcaagagagt gttggtcaac tgccttc

47

7 6 / 1 4 3

<210> 60

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 60

tcccccteta cctgtccagc atgttcaaga gacatgctgg acaggtagag g

51

<210> 61

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 61

aaaaccteta cctgtccagc atgtctcttg aacatgctgg acaggtagag g

51

7 7 / 1 4 3

<210> 62

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for hairpin
siRNA

<400> 62

cctctacctg tccagcatgt tcaagagaca tgctggacag gtagagg

47

<210> 63

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 63

tcccgttcac cagcgccatc tggttcaaga gaccagatgg cgctgatgaa c

51

7 8 / 1 4 3

<210> 64

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 64

aaaagttcat cagcgccatc tggctctcttg aaccagatgg cgctgatgaa c

51

<210> 65

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for hairpin
siRNA

<400> 65

gttcatcagc gccatctggt tcaagagacc agatggcgct gatgaac

47

7 9 / 1 4 3

<210> 66

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 66

tcccggtcgt catcacggtc aacttcaaga gagttgacct gtatgaacgac c

51

<210> 67

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for
construction of siRNA expression vector

<400> 67

aaaaggtcgt catcacggtc aactctcttg aagttgacct gtatgaacgac c

51

8 0 / 1 4 3

<210> 68

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for hairpin
siRNA

<400> 68

ggctgcata caggtcaact tcaagagagt tgacctgtat gacgacc

47

<210> 69

<211> 20

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 69

atgaacaaac tgtatatcgg

20

8 1 / 1 4 3

<210> 70

<211> 18

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 70

cttcggttt gactgagg

18

<210> 71

<211> 20

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 71

atgaacaaac tgtatatcgg

20

8 2 / 1 4 3

<210> 72

<211> 19

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 72

atgagettca agtttcacc

19

<210> 73

<211> 20

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 73

atgaacaaac tgttatatcg

20

8 3 / 1 4 3

<210> 74

<211> 18

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 74

ctccgtttct gattgctc

18

<210> 75

<211> 20

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 75

atgaacaaac tgtatatcgg

20

8 4 / 1 4 3

<210> 76

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 76

aggcaaatca catggtttct g

21

<210> 77

<211> 18

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 77

ttgcctctgc gectgctg

18

8 5 / 1 4 3

<210> 78

<211> 18

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 78

cttcgctctt gactgagg

18

<210> 79

<211> 18

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 79

ttgcctctgc gcctgctg

18

8 6 / 1 4 3

<210> 80

<211> 18

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for construction of
IMP-3 deletion mutant

<400> 80

ctccgtttct gattgctc

18

<210> 81

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 81

ttatcctgaa cagctctttg gtg

23

<210> 82

8 7 / 1 4 3

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 82

aagcgaaggt cagctaaata tcc

23

<210> 83

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 83

ctttctgagc acactacgga tct

23

<210> 84

<211> 23

<212> DNA

8 8 / 1 4 3

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 84

aagccctctt acttacaggg aaa

23

<210> 85

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 85

ggttccctg gatttagtga a

21

<210> 86

<211> 25

<212> DNA

<213> Artificial

8 9 / 1 4 3

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 86

caacagtaaa tctgaaactc ttgcc

25

<210> 87

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 87

gacaaaggta gcaagaggat ttc

23

<210> 88

<211> 22

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

9 0 / 1 4 3

<400> 88

ctggtgttaa actcggttct tc

22

<210> 89

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 89

ctagtgagtg aggctattgc agc

23

<210> 90

<211> 24

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 90

9 1 / 1 4 3

gtctcttcteta gcacctcaat ctcc

24

<210> 91

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 91

atctgacttt ctgtccactg cat

23

<210> 92

<211> 22

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 92

taattcagca taagccaaag cc

22

9 2 / 1 4 3

<210> 93

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 93

acacagtatg gactgaaatc gac

23

<210> 94

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 94

cacctcaatc tgaacaaggt tag

23

<210> 95

9 3 / 1 4 3

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 95

ggcctctcaa agtctggttag att

23

<210> 96

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for IP-RT-PCR

<400> 96

atatccac ttcagagacg aca

23

<210> 97

<211> 197

<212> PRT

9 4 / 1 4 3

<213> Artificial

<220>

<223> An artificially synthesized sequence of IMP-3 deletion mutant

<400> 97

Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser

1 5 10 15

Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro

20 25 30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser

35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His

50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile

65 70 75 80

9 5 / 1 4 3

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
85 90 95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
100 105 110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
115 120 125

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
165 170 175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys

9 6 / 1 4 3

180

185

190

Pro Cys Asp Leu Pro

195

<210> 98

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for Quantitative
RT-PCR

<400> 98

acgaactcat ttgctcactc ctt

23

<210> 99

<211> 21

<212> DNA

<213> Artificial

<220>

9 7 / 1 4 3

<223> An artificially synthesized primer sequence for Quantitative
RT-PCR

<400> 99

accacacccc aacacaattg t

21

<210> 100

<211> 12

<212> DNA

<213> Artificial

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<223> An artificially synthesized primer sequence for Quantitative
RT-PCR

<400> 100

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12

<210> 101

<211> 23

<212> DNA

<213> Artificial

<220>

9 8 / 1 4 3

<223> An artificially synthesized primer sequence for Quantitative
RT-PCR

<400> 101

ttcacccctga cagagttcac aaa

23

<210> 102

<211> 22

<212> DNA

<213> Artificial

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<223> An artificially synthesized primer sequence for Quantitative
RT-PCR

<400> 102

gggtggtctc ccataatagc aa

22

<210> 103

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<213> Artificial

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99/143

<223> An artificially synthesized primer sequence for Quantitative
RT-PCR

<400> 103

agcccacttt agagtatac

19

<210> 104

<211> 4168

<212> DNA

<213> Homo sapiens

<400> 104

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ttcttggtgt tggttcttac tgtgttttg tattttaaag gcgagaagac gaggggaaca 180

aaaccagctg gatccatcca tcacgtggg tggttttaat tttctgtttt ttctcgttat 240

ttttttttaa acaaccactc ttcacaatga acaaactgta tatcggaac ctacagcaga 300

acgcgcgcc ctcggacctg gaaagtatct tcaaggacgc caagatcccg gtgtcgggac 360

ccttcttggt gaagactggc tacgcgttcg tggactgccc ggacgagagc tgggcctca 420

1 0 0 / 1 4 3

aggccatcga ggcgctttca ggtaaaatag aactgcacgg gaaacccata gaagttgagc 480

actcggctccc aaaaaggcaa aggattcgga aacttcagat acgaaatata ccgcctcatt 540

tacagtggga ggtgctggat agtttactag tccagtatgg agtgggtggag agctgtgagc 600

aagtgaacac tgactcgga actgcagttg taaatgtaac ctattccagt aaggaccaag 660

ctagacaagc actagacaaa ctgaatggat ttcagttaga gaatttcacc ttgaaagtag 720

cctatatccc tgatgaaatg gccgcccagc aaaacccctt gcagcagccc cgaggctgcc 780

gggggcttgg gcagaggggc tctcaaggc aggggtctcc aggatccgta tccaagcaga 840

aaccatgtga tttgcctctg cgcctgctgg tteccacca atttgttga gccatcatag 900

gaaaagaagg tgccaccatt cggaacatca ccaaacagac ccagtctaaa atcgatgtcc 960

accgtaaaga aaatgcgggg gctgctgaga agtcgattac tatcctctct actcctgaag 1020

gcacctctgc ggcttgaag tctattctgg agattatgca taaggaaagt caagatataa 1080

aattcacaga agagatcccc ttgaagattt tagctcataa taactttgtt ggacgtctta 1140

ttggtaaaga aggaagaaat citaaaaaaa ttgagcaaga cacagacact aaatcacga 1200

1 0 1 / 1 4 3

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atgttgagac atgtgcaaaa gctgaggagg agatcatgaa gaaaatcagg gagtcttatg 1320

aaaatgatat tgcttttatg aatcttcaag cacatttaat tcctggatta aatctgaacg 1380

ccttgggtct gttccacccc acttcaggga tgccacctcc cacctcaggg ccccttcag 1440

ccatgactcc tccctaccog cagtttgagc aatcagaaac ggagactgtt catctgttta 1500

tcccagctct atcagtcggt gccatcatcg gcaagcaggg ccagcacatc aagcagcttt 1560

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gaaaaattaa agaagaaaac ttgttagtc ctaaagaaga ggtgaaactt gaagtcata 1740

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aacttcagaa ttgtcaagt gcagaagttg ttgtccctcg tgaccagaca cctgatgaga 1860

atgaccaagt ggttgtcaaa ataactggtc acttctatgc ttgccaggtt gccagagaa 1920

aaattcagga aattctgact caggtaaagc agcaccaaca acagaaggct ctgcaaagtg 1980

1 0 2 / 1 4 3

gaccacctca gtcaagacgg aagtaaagcg tcaggaaaca gccaccaca gaggcagatg 2040

ccaaacaaaa gacagattgc ttaaccaaca gatgggcgct gacccctat ccagaatcac 2100

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1 0 3 / 1 4 3

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gcctagtatc tggagagcag cactaccatt tattctttca ttatagttg ggaaagtttt 2880

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1 0 4 / 1 4 3

gatctaaagg acatatatat aaccctttaa aaaaaaaatc actgcctcat tcttatttca 3600

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<210> 105

<211> 579

1 0 5 / 1 4 3

<212> PRT

<213> Homo sapiens

<400> 105

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Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro

20 25 30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser

35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His

50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile

65 70 75 80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val

1 0 6 / 1 4 3

85

90

95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln

100

105

110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser

115

120

125

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu

130

135

140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala

145

150

155

160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln

165

170

175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys

180

185

190

1 0 7 / 1 4 3

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
195 200 205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
210 215 220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
225 230 235 240

Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
245 250 255

Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
260 265 270

Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
275 280 285

Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Ile Glu Gln

1 0 8 / 1 4 3

290

295

300

Asp Thr Asp Thr Lys Ile Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu

305

310

315

320

Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys

325

330

335

Ala Lys Ala Glu Glu Glu Ile Met Lys Lys Ile Arg Glu Ser Tyr Glu

340

345

350

Asn Asp Ile Ala Ser Met Asn Leu Gln Ala His Leu Ile Pro Gly Leu

355

360

365

Asn Leu Asn Ala Leu Gly Leu Phe Pro Pro Thr Ser Gly Met Pro Pro

370

375

380

Pro Thr Ser Gly Pro Pro Ser Ala Met Thr Pro Pro Tyr Pro Gln Phe

385

390

395

400

1 0 9 / 1 4 3

Glu Gln Ser Glu Thr Glu Thr Val His Leu Phe Ile Pro Ala Leu Ser

405

410

415

Val Gly Ala Ile Ile Gly Lys Gln Gly Gln His Ile Lys Gln Leu Ser

420

425

430

Arg Phe Ala Gly Ala Ser Ile Lys Ile Ala Pro Ala Glu Ala Pro Asp

435

440

445

Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe

450

455

460

Lys Ala Gln Gly Arg Ile Tyr Gly Lys Ile Lys Glu Glu Asn Phe Val

465

470

475

480

Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser

485

490

495

Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu

1 1 0 / 1 4 3

500

505

510

Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr

515

520

525

Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr

530

535

540

Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val

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555

560

Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser

565

570

575

Arg Arg Lys

<210> 106

<211> 3487

<212> DNA

1 1 1 / 1 4 3

<213> Homo sapiens

<220>

<221> CDS

<222> (266)..(2512)

<400> 106

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gccccgtcc ggggccctgg ctccgcccc aggttgagg agcccgagc ccgccttcgg 180

agctacggcc taacggcggc ggcgactgca gtctggaggg tccacattg tgatttcaa 240

tggagagtga aaacgcagat tcata atg aaa act agc ccc cgt cgg cca ctg 292

Met Lys Thr Ser Pro Arg Arg Pro Leu

1

5

att ctc aaa aga cgg agg ctg ccc ctt cct gtt caa aat gcc cca agt 340

Ile Leu Lys Arg Arg Arg Leu Pro Leu Pro Val Gln Asn Ala Pro Ser

10

15

20

25

gaa aca tca gag gag gaa cct aag aga tcc cct gcc caa cag gag tct 388

Glu Thr Ser Glu Glu Glu Pro Lys Arg Ser Pro Ala Gln Gln Glu Ser

1 1 2 / 1 4 3

30

35

40

aat caa gca gag gcc tcc aag gaa gtg gca gag tcc aac tct tgc aag 436
 Asn Gln Ala Glu Ala Ser Lys Glu Val Ala Glu Ser Asn Ser Cys Lys

45

50

55

ttt cca gct ggg atc aag att att aac cac ccc acc atg ccc aac acg 484
 Phe Pro Ala Gly Ile Lys Ile Ile Asn His Pro Thr Met Pro Asn Thr

60

65

70

caa gta gtg gcc atc ccc aac aat gct aat att cac agc atc atc aca 532
 Gln Val Val Ala Ile Pro Asn Asn Ala Asn Ile His Ser Ile Ile Thr

75

80

85

gca ctg act gcc aag gga aaa gag agt ggc agt agt ggg ccc aac aaa 580
 Ala Leu Thr Ala Lys Gly Lys Glu Ser Gly Ser Ser Gly Pro Asn Lys

90

95

100

105

ttc atc ctc atc agc tgt ggg gga gcc cca act cag cct cca gga ctc 628
 Phe Ile Leu Ile Ser Cys Gly Gly Ala Pro Thr Gln Pro Pro Gly Leu

110

115

120

cgg cct caa acc caa acc agc tat gat gcc aaa agg aca gaa gtg acc 676
 Arg Pro Gln Thr Gln Thr Ser Tyr Asp Ala Lys Arg Thr Glu Val Thr

125

130

135

1 1 3 / 1 4 3

ctg gag acc ttg gga cca aaa cct gca gct agg gat gtg aat ctt cct 724
 Leu Glu Thr Leu Gly Pro Lys Pro Ala Ala Arg Asp Val Asn Leu Pro
 140 145 150

aga cca cct gga gcc ctt tgc gag cag aaa cgg gag acc tgt gca gat 772
 Arg Pro Pro Gly Ala Leu Cys Glu Gln Lys Arg Glu Thr Cys Ala Asp
 155 160 165

ggt gag gca gca ggc tgc act atc aac aat agc cta tcc aac atc cag 820
 Gly Glu Ala Ala Gly Cys Thr Ile Asn Asn Ser Leu Ser Asn Ile Gln
 170 175 180 185

tgg ctt cga aag atg agt tct gat gga ctg ggc tcc cgc agc atc aag 868
 Trp Leu Arg Lys Met Ser Ser Asp Gly Leu Gly Ser Arg Ser Ile Lys
 190 195 200

caa gag atg gag gaa aag gag aat tgt cac ctg gag cag cga cag gtt 916
 Gln Glu Met Glu Glu Lys Glu Asn Cys His Leu Glu Gln Arg Gln Val
 205 210 215

aag gtt gag gag cct tcg aga cca tca gcg tcc tgg cag aac tct gtg 964
 Lys Val Glu Glu Pro Ser Arg Pro Ser Ala Ser Trp Gln Asn Ser Val
 220 225 230

tct gag cgg cca ccc tac tct tac atg gcc atg ata caa ttc gcc atc 1012
 Ser Glu Arg Pro Pro Tyr Ser Tyr Met Ala Met Ile Gln Phe Ala Ile

1 1 4 / 1 4 3

235	240	245	
aac agc act gag agg aag cgc atg act ttg aaa gac atc tat acg tgg			1060
Asn Ser Thr Glu Arg Lys Arg Met Thr Leu Lys Asp Ile Tyr Thr Trp			
250	255	260	265
att gag gac cac ttt ccc tac ttt aag cac att gcc aag cca ggc tgg			1108
Ile Glu Asp His Phe Pro Tyr Phe Lys His Ile Ala Lys Pro Gly Trp			
	270	275	280
aag aac tcc atc cgc cac aac ctt tcc ctg cac gac atg ttt gtc cgg			1156
Lys Asn Ser Ile Arg His Asn Leu Ser Leu His Asp Met Phe Val Arg			
285	290	295	
gag acg tct gcc aat ggc aag gtc tcc ttc tgg acc att cac ccc agt			1204
Glu Thr Ser Ala Asn Gly Lys Val Ser Phe Trp Thr Ile His Pro Ser			
300	305	310	
gcc aac cgc tac ttg aca ttg gac cag gtg ttt aag cag cag aaa cga			1252
Ala Asn Arg Tyr Leu Thr Leu Asp Gln Val Phe Lys Gln Gln Lys Arg			
315	320	325	
ccg aat cca gag ctc cgc cgg aac atg acc atc aaa acc gaa ctc ccc			1300
Pro Asn Pro Glu Leu Arg Arg Asn Met Thr Ile Lys Thr Glu Leu Pro			
330	335	340	345

1 1 5 / 1 4 3

ctg ggc gca cgg cgg aag atg aag cca ctg cta cca cgg gtc agc tca 1348
Leu Gly Ala Arg Arg Lys Met Lys Pro Leu Leu Pro Arg Val Ser Ser
350 355 360

tac ctg gta cct atc cag ttc ccg gtg aac cag tca ctg gtg ttg cag 1396
Tyr Leu Val Pro Ile Gln Phe Pro Val Asn Gln Ser Leu Val Leu Gln
365 370 375

ccc tcg gtg aag gtg cca ttg ccc ctg gcg gct tcc ctc atg agc tca 1444
Pro Ser Val Lys Val Pro Leu Pro Leu Ala Ala Ser Leu Met Ser Ser
380 385 390

gag ctt gcc cgc cat agc aag cga gtc cgc att gcc ccc aag gtg ctg 1492
Glu Leu Ala Arg His Ser Lys Arg Val Arg Ile Ala Pro Lys Val Leu
395 400 405

cta gct gag gag ggg ata gct cct ctt tct tct gca gga cca ggg aaa 1540
Leu Ala Glu Glu Gly Ile Ala Pro Leu Ser Ser Ala Gly Pro Gly Lys
410 415 420 425

gag gag aaa ctc ctg ttt gga gaa ggg ttt tct cct ttg ctt cca gtt 1588
Glu Glu Lys Leu Leu Phe Gly Glu Gly Phe Ser Pro Leu Leu Pro Val
430 435 440

cag act atc aag gag gaa gaa atc cag cct ggg gag gaa atg cca cac 1636
Gln Thr Ile Lys Glu Glu Glu Ile Gln Pro Gly Glu Glu Met Pro His

1 1 6 / 1 4 3

445	450	455	
tta gcg aga ccc atc aaa gtg gag agc cct ccc ttg gaa gag tgg ccc			1684
Leu Ala Arg Pro Ile Lys Val Glu Ser Pro Pro Leu Glu Glu Trp Pro			
460	465	470	
tcc ccg gcc cca tct ttc aaa gag gaa tca tct cac tcc tgg gag gat			1732
Ser Pro Ala Pro Ser Phe Lys Glu Glu Ser Ser His Ser Trp Glu Asp			
475	480	485	
tcg tcc caa tct ccc acc cca aga ccc aag aag tcc tac agt ggg ctt			1780
Ser Ser Gln Ser Pro Thr Pro Arg Pro Lys Lys Ser Tyr Ser Gly Leu			
490	495	500	505
agg tcc cca acc cgg tgt gtc tcg gaa atg ctt gtg att caa cac agg			1828
Arg Ser Pro Thr Arg Cys Val Ser Glu Met Leu Val Ile Gln His Arg			
510	515	520	
gag agg agg gag agg agc cgg tct cgg agg aaa cag cat cta ctg cct			1876
Glu Arg Arg Glu Arg Ser Arg Ser Arg Arg Lys Gln His Leu Leu Pro			
525	530	535	
ccc tgt gtg gat gag ccg gag ctg ctc ttc tca gag ggg ccc agt act			1924
Pro Cys Val Asp Glu Pro Glu Leu Leu Phe Ser Glu Gly Pro Ser Thr			
540	545	550	

1 1 7 / 1 4 3

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Ser Arg Trp Ala Ala Glu Leu Pro Phe Pro Ala Asp Ser Ser Asp Pro
555 560 565

gcc tcc cag ctc agc tac tcc cag gaa gtg gga gga cct ttt aag aca 2020
Ala Ser Gln Leu Ser Tyr Ser Gln Glu Val Gly Gly Pro Phe Lys Thr
570 575 580 585

ccc att aag gaa acg ctg ccc atc tcc tcc acc ccg agc aaa tct gtc 2068
Pro Ile Lys Glu Thr Leu Pro Ile Ser Ser Thr Pro Ser Lys Ser Val
590 595 600

ctc ccc aga acc cct gaa tcc tgg agg ctc acg ccc cca gcc aaa gta 2116
Leu Pro Arg Thr Pro Glu Ser Trp Arg Leu Thr Pro Pro Ala Lys Val
605 610 615

ggg gga ctg gat ttc agc cca gta caa acc tcc cag ggt gcc tct gac 2164
Gly Gly Leu Asp Phe Ser Pro Val Gln Thr Ser Gln Gly Ala Ser Asp
620 625 630

ccc ttg cct gac ccc ctg ggg ctg atg gat ctc agc acc act ccc ttg 2212
Pro Leu Pro Asp Pro Leu Gly Leu Met Asp Leu Ser Thr Thr Pro Leu
635 640 645

caa agt get ccc ccc ctt gaa tca ccg caa agg ctc ctc agt tca gaa 2260
Gln Ser Ala Pro Pro Leu Glu Ser Pro Gln Arg Leu Leu Ser Ser Glu

1 1 8 / 1 4 3

650

655

660

665

ccc tta gac ctc atc tcc gtc ccc ttt ggc aac tct tct ccc tca gat 2308

Pro Leu Asp Leu Ile Ser Val Pro Phe Gly Asn Ser Ser Pro Ser Asp

670

675

680

ata gac gtc ccc aag cca ggc tcc ccg gag cca cag gtt tct ggc ctt 2356

Ile Asp Val Pro Lys Pro Gly Ser Pro Glu Pro Gln Val Ser Gly Leu

685

690

695

gca gcc aat cgt tct ctg aca gaa ggc ctg gtc ctg gac aca atg aat 2404

Ala Ala Asn Arg Ser Leu Thr Glu Gly Leu Val Leu Asp Thr Met Asn

700

705

710

gac agc ctc agc aag atc ctg ctg gac atc agc ttt cct ggc ctg gac 2452

Asp Ser Leu Ser Lys Ile Leu Leu Asp Ile Ser Phe Pro Gly Leu Asp

715

720

725

gag gac cca ctg ggc cct gac aac atc aac tgg tcc cag ttt att cct 2500

Glu Asp Pro Leu Gly Pro Asp Asn Ile Asn Trp Ser Gln Phe Ile Pro

730

735

740

745

gag cta cag tag agccctgcc ttgccctgt gctcaagctg tccaccatcc 2552

Glu Leu Gln

1 1 9 / 1 4 3

cgggcactcc aaggetcagt gcacccaag cctctgagtg aggacagcag gcagggactg 2612

ttctgtcct catagctccc tgctgcctga ttatgcaaaa gtagcagtca caccctagcc 2672

actgtcggga ctttgtgttc cccaagagta tctgattcct ctgtgtcccc tgccaggagc 2732

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gcaactgaag cagagtgtgg gtgccagat gtgcgtatt agatgtttct ctgataatgt 3272

ccccaatcat accagggaga ctggcattga cgagaactca ggtggaggct tgagaaggcc 3332

1 2 0 / 1 4 3

gaaagggccc ctgacctgcc tggtttcett agcttgcccc tcagctttgc aaagagccac 3392

cctagggccc agctgaccgc atgggtgtga gccagcttga gaacactaac tactcaataa 3452

aagcgaaggt ggacaaaaaa aaaaaaaaaa aaaaa 3487

<210> 107

<211> 748

<212> PRT

<213> Homo sapiens

<400> 107

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1

5

10

15

Pro Leu Pro Val Gln Asn Ala Pro Ser Glu Thr Ser Glu Glu Glu Pro

20

25

30

Lys Arg Ser Pro Ala Gln Gln Glu Ser Asn Gln Ala Glu Ala Ser Lys

35

40

45

1 2 1 / 1 4 3

Glu Val Ala Glu Ser Asn Ser Cys Lys Phe Pro Ala Gly Ile Lys Ile

50

55

60

Ile Asn His Pro Thr Met Pro Asn Thr Gln Val Val Ala Ile Pro Asn

65

70

75

80

Asn Ala Asn Ile His Ser Ile Ile Thr Ala Leu Thr Ala Lys Gly Lys

85

90

95

Glu Ser Gly Ser Ser Gly Pro Asn Lys Phe Ile Leu Ile Ser Cys Gly

100

105

110

Gly Ala Pro Thr Gln Pro Pro Gly Leu Arg Pro Gln Thr Gln Thr Ser

115

120

125

Tyr Asp Ala Lys Arg Thr Glu Val Thr Leu Glu Thr Leu Gly Pro Lys

130

135

140

Pro Ala Ala Arg Asp Val Asn Leu Pro Arg Pro Pro Gly Ala Leu Cys

145

150

155

160

1 2 2 / 1 4 3

Glu Gln Lys Arg Glu Thr Cys Ala Asp Gly Glu Ala Ala Gly Cys Thr
165 170 175

Ile Asn Asn Ser Leu Ser Asn Ile Gln Trp Leu Arg Lys Met Ser Ser
180 185 190

Asp Gly Leu Gly Ser Arg Ser Ile Lys Gln Glu Met Glu Glu Lys Glu
195 200 205

Asn Cys His Leu Glu Gln Arg Gln Val Lys Val Glu Glu Pro Ser Arg
210 215 220

Pro Ser Ala Ser Trp Gln Asn Ser Val Ser Glu Arg Pro Pro Tyr Ser
225 230 235 240

Tyr Met Ala Met Ile Gln Phe Ala Ile Asn Ser Thr Glu Arg Lys Arg
245 250 255

1 2 3 / 1 4 3

Met Thr Leu Lys Asp Ile Tyr Thr Trp Ile Glu Asp His Phe Pro Tyr

260

265

270

Phe Lys His Ile Ala Lys Pro Gly Trp Lys Asn Ser Ile Arg His Asn

275

280

285

Leu Ser Leu His Asp Met Phe Val Arg Glu Thr Ser Ala Asn Gly Lys

290

295

300

Val Ser Phe Trp Thr Ile His Pro Ser Ala Asn Arg Tyr Leu Thr Leu

305

310

315

320

Asp Gln Val Phe Lys Gln Gln Lys Arg Pro Asn Pro Glu Leu Arg Arg

325

330

335

Asn Met Thr Ile Lys Thr Glu Leu Pro Leu Gly Ala Arg Arg Lys Met

340

345

350

Lys Pro Leu Leu Pro Arg Val Ser Ser Tyr Leu Val Pro Ile Gln Phe

355

360

365

1 2 4 / 1 4 3

Pro Val Asn Gln Ser Leu Val Leu Gln Pro Ser Val Lys Val Pro Leu
370 375 380

Pro Leu Ala Ala Ser Leu Met Ser Ser Glu Leu Ala Arg His Ser Lys
385 390 395 400

Arg Val Arg Ile Ala Pro Lys Val Leu Leu Ala Glu Glu Gly Ile Ala
405 410 415

Pro Leu Ser Ser Ala Gly Pro Gly Lys Glu Glu Lys Leu Leu Phe Gly
420 425 430

Glu Gly Phe Ser Pro Leu Leu Pro Val Gln Thr Ile Lys Glu Glu Glu
435 440 445

Ile Gln Pro Gly Glu Glu Met Pro His Leu Ala Arg Pro Ile Lys Val
450 455 460

1 2 5 / 1 4 3

Glu Ser Pro Pro Leu Glu Glu Trp Pro Ser Pro Ala Pro Ser Phe Lys
465 470 475 480

Glu Glu Ser Ser His Ser Trp Glu Asp Ser Ser Gln Ser Pro Thr Pro
485 490 495

Arg Pro Lys Lys Ser Tyr Ser Gly Leu Arg Ser Pro Thr Arg Cys Val
500 505 510

Ser Glu Met Leu Val Ile Gln His Arg Glu Arg Arg Glu Arg Ser Arg
515 520 525

Ser Arg Arg Lys Gln His Leu Leu Pro Pro Cys Val Asp Glu Pro Glu
530 535 540

Leu Leu Phe Ser Glu Gly Pro Ser Thr Ser Arg Trp Ala Ala Glu Leu
545 550 555 560

Pro Phe Pro Ala Asp Ser Ser Asp Pro Ala Ser Gln Leu Ser Tyr Ser
565 570 575

1 2 6 / 1 4 3

Gln Glu Val Gly Gly Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro
580 585 590

Ile Ser Ser Thr Pro Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser
595 600 605

Trp Arg Leu Thr Pro Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro
610 615 620

Val Gln Thr Ser Gln Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly
625 630 635 640

Leu Met Asp Leu Ser Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu
645 650 655

Ser Pro Gln Arg Leu Leu Ser Ser Glu Pro Leu Asp Leu Ile Ser Val
660 665 670

1 2 7 / 1 4 3

Pro Phe Gly Asn Ser Ser Pro Ser Asp Ile Asp Val Pro Lys Pro Gly

675

680

685

Ser Pro Glu Pro Gln Val Ser Gly Leu Ala Ala Asn Arg Ser Leu Thr

690

695

700

Glu Gly Leu Val Leu Asp Thr Met Asn Asp Ser Leu Ser Lys Ile Leu

705

710

715

720

Leu Asp Ile Ser Phe Pro Gly Leu Asp Glu Asp Pro Leu Gly Pro Asp

725

730

735

Asn Ile Asn Trp Ser Gln Phe Ile Pro Glu Leu Gln

740

745

<210> 108

<211> 19

<212> DNA

<213> Artificial

<220>

1 2 8 / 1 4 3

<223> A target sequence for siRNA.

<400> 108

gcagcagaaa cgaccgaat

19

<210> 109

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 109

tccgcagca gaaacgaccg aatttcaaga gaattcggtc gtttctgctg c

51

<210> 110

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA.

1 2 9 / 1 4 3

<400> 110

aaaagcagca gaaacgaccg aattctcttg aaattcggtc gtttctgtg c

51

<210> 111

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized hairpin siRNA sequence.

<400> 111

gcagcagaaa cgaccgaatt tcaagagaat tcggtcggtt ctgtgc

47

<210> 112

<211> 2931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146)..(751)

1 3 0 / 1 4 3

<400> 112

agggggagcg gagggaggtg ttctgtcag ttccggctgt ttgttcggga agtggatccg 60

ccgctgccgg agcagcccca agggagctgc ggcgcgcgag gccagtaccg accccgcccg 120

ccgcgcgcga ccgccccgc ccgcc atg gcc cgg gac tac gac cac ctc ttc 172

Met Ala Arg Asp Tyr Asp His Leu Phe

1

5

aag ctg ctc atc atc ggc gac agc ggt gtg ggc aag agc agt tta ctg 220

Lys Leu Leu Ile Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Leu

10

15

20

25

ttg cgt ttt gca gac aac act ttc tca ggc agc tac atc acc acg atc 268

Leu Arg Phe Ala Asp Asn Thr Phe Ser Gly Ser Tyr Ile Thr Thr Ile

30

35

40

gga gtg gat ttc aag atc cgg acc gtg gag atc aac ggg gag aag gtg 316

Gly Val Asp Phe Lys Ile Arg Thr Val Glu Ile Asn Gly Glu Lys Val

45

50

55

aag ctg cag atc tgg gac aca gcg ggg cag gag cgc ttc cgc acc atc 364

Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile

60

65

70

acc tcc acg tat tat cgg ggg acc cac ggg gtc att gtg gtt tac gac 412

1 3 1 / 1 4 3

Thr Ser Thr Tyr Tyr Arg Gly Thr His Gly Val Ile Val Val Tyr Asp

75

80

85

gtc acc agt gcc gag tcc ttt gtc aac gtc aag cgg tgg ctt cac gaa 460

Val Thr Ser Ala Glu Ser Phe Val Asn Val Lys Arg Trp Leu His Glu

90

95

100

105

atc aac cag aac tgt gat gat gtg tgc cga ata tta gtg ggt aat aag 508

Ile Asn Gln Asn Cys Asp Asp Val Cys Arg Ile Leu Val Gly Asn Lys

110

115

120

aat gac gac cct gag cgg aag gtg gtg gag acg gaa gat gcc tac aaa 556

Asn Asp Asp Pro Glu Arg Lys Val Val Glu Thr Glu Asp Ala Tyr Lys

125

130

135

ttc gcc ggg cag atg ggc atc cag ttg ttc gag acc agc gcc aag gag 604

Phe Ala Gly Gln Met Gly Ile Gln Leu Phe Glu Thr Ser Ala Lys Glu

140

145

150

aat gtc aac gtg gaa gag atg ttc aac tgc atc acg gag ctg gtc ctc 652

Asn Val Asn Val Glu Glu Met Phe Asn Cys Ile Thr Glu Leu Val Leu

155

160

165

cga gca aag aaa gac aac ctg gca aaa cag cag cag caa caa cag aac 700

Arg Ala Lys Lys Asp Asn Leu Ala Lys Gln Gln Gln Gln Gln Asn

170

175

180

185

1 3 2 / 1 4 3

gat gtg gtg aag ctc acg aag aac agt aaa cga aag aaa cgc tgc tgc	748
Asp Val Val Lys Leu Thr Lys Asn Ser Lys Arg Lys Lys Arg Cys Cys	
190 195 200	
taa tggcaccag tccactgcag agactgcact gcggtccctc cccagcccg	801
aggccacagg aggttcctcg ggggacagtc tcagtttcgt gccgttattt aaagaattct	861
ctccatgttt ttgtatcggg aggtgccatc ggcacttcct ccccgcct cctcagtg	921
caagaagggt ttggaccagc ccgcccttc ctactggtgc cccctcctc ccggccaagg	981
gcctggacc tggcgaggac gctgcccgcc gagcggactg attcgcagag tetgtacata	1041
gtgtatatgt ctctaccggc ccgcacacca cgtcctgctc tggtttttgc etttctgatg	1101
ccagcctgct gcaacagacc ctccccgcgc cctccccag cccatcttac tgcaagcagc	1161
gtcctgagga gacagcggca cgttctagct gcgtctgcgg ccagcccggt ccagtgaggat	1221
gggtcccggt ttgtcattc tctccgacag gttgtcagcc tetgtccccc ctgcacaggg	1281
tcttgccctt tctccggggc ctgtgccagc tcccttcctt ccccgttgtc ctgtccccc	1341
agccattctg ggagctgggg aacctggtct caaggcaggc cctgcagttc cacagaggtg	1401

1 3 3 / 1 4 3

gcaggtcttg ccccttggcc aacagatttc ttgtcctgcc ttctagatgc ctctgagetc 1461

caaaccagg gcagccatgg cttctcattt acaccaacag gtttcagttc caacagaaag 1521

gtcgggtag gttcgtgcag agatggggct ggcagggggg ctatgggagg attatttta 1581

cagatcaaga aaatgaagcc aaatcaagt aattaaattc ctcaaatata tttcttttc 1641

ctgaggtttg attggcacag cagcaaaagt tgaggccacc ccaatttgtt ccaactgttt 1701

tagaaaaaa tgaatggctt cctgccattg tggggctgga ctcttgggct ttcttggtgg 1761

gagcggagaa ggggcctccc acccttgtcc gagttgctc ccactggagg tcaggagtct 1821

acactgcagc ctccggcact gtggggagtg catgcctggg gcctctgggt ggggaccatg 1881

gacaggccct ggtcactgtc ctaacctttg tcaggacaaa ggtagcaaga ggatttctg 1941

gcgggtggga aggaatggct ggggcggcca gttttgacac gcccagtg cctggagaac 2001

aaccaggctc atctgcactt gatgactgct ccccgacccc cagcccgagc acctcattcc 2061

cctccacta cagggatcaa gtgacctggg aagaaccgag tttaacacca ggatgtgttt 2121

ccttagattt cctttcctag gcgatttcca gggagagccc tgattggaca atcacatcac 2181

1 3 4 / 1 4 3

agatcacact gcagtttcca tgtagcact gtgatgggt ttttaataca taaaaactgg 2241

gggtttcttc tcaccgactc tcacttgcc caaactgcc aaagctggtg attctgggac 2301

aggccttcac ttggagcca cgggatgggg tgggggagcc ccatgggcct gggaaggagg 2361

gtgctgtgga gggggctgca gggctgacca gcaggcagcc tcactgtgtc gggggcgggg 2421

gcggcaggag cagaagcggg gtctccgtcc ttgggactgt cctggttgcc caccggccct 2481

gaggatgcac ggtgcctggg gtctctgtgc cgtggggcgg ggggcatgct ggcctctgag 2541

cgatcaggcg aggccagcga ggggtgtgctt gcaaattcaa gcaataagag gggggttcct 2601

gggggcttcc agcccaggct agaagccccc atggcttctg gcagctggac atcagcccca 2661

ggtattgggg tgattttggt catgacagtg tgccgtgtccc actgttacac gcataaatgg 2721

gggttatggg gtgggggtgg ggactcaggg ctggaccgac gtccatgtgg acctgatgtg 2781

aaattcctgt caaacaaca ccaactttta atggtttgct aggagtattt ctgtattgaa 2841

agtttctaata tatgcttttt aaaaaatac taaaaataaa ggttcaagct gccaaaaaaa 2901

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2931

1 3 5 / 1 4 3

<210> 113

<211> 201

<212> PRT

<213> Homo sapiens

<400> 113

Met Ala Arg Asp Tyr Asp His Leu Phe Lys Leu Leu Ile Ile Gly Asp

1

5

10

15

Ser Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Ala Asp Asn Thr

20

25

30

Phe Ser Gly Ser Tyr Ile Thr Thr Ile Gly Val Asp Phe Lys Ile Arg

35

40

45

Thr Val Glu Ile Asn Gly Glu Lys Val Lys Leu Gln Ile Trp Asp Thr

50

55

60

Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Thr Tyr Tyr Arg Gly

1 3 6 / 1 4 3

65

70

75

80

Thr His Gly Val Ile Val Val Tyr Asp Val Thr Ser Ala Glu Ser Phe

85

90

95

Val Asn Val Lys Arg Trp Leu His Glu Ile Asn Gln Asn Cys Asp Asp

100

105

110

Val Cys Arg Ile Leu Val Gly Asn Lys Asn Asp Asp Pro Glu Arg Lys

115

120

125

Val Val Glu Thr Glu Asp Ala Tyr Lys Phe Ala Gly Gln Met Gly Ile

130

135

140

Gln Leu Phe Glu Thr Ser Ala Lys Glu Asn Val Asn Val Glu Glu Met

145

150

155

160

Phe Asn Cys Ile Thr Glu Leu Val Leu Arg Ala Lys Lys Asp Asn Leu

165

170

175

1 3 7 / 1 4 3

Ala Lys Gln Gln Gln Gln Gln Gln Asn Asp Val Val Lys Leu Thr Lys
180 185 190

Asn Ser Lys Arg Lys Lys Arg Cys Cys
195 200

<210> 114

<211> 19

<212> DNA

<213> Artificial

<220>

<223> A target sequence for siRNA.

<400> 114

gagatgttca actgcatca

19

<210> 115

<211> 51

<212> DNA

<213> Artificial

1 3 8 / 1 4 3

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 115

tcccagatg ttcaactgca tcattcaaga gatgatgcag ttgaacatct c 51

<210> 116

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 116

aaaagagatg ttcaactgca tcattctcttg aatgatgcag ttgaacatct c 51

<210> 117

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized hairpin siRNA sequence.

1 3 9 / 1 4 3

<400> 117

gagatgttca actgcatcat tcaagagatg atgcagttga acatctc

47

<210> 118

<211> 22

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 118

aaaaaggga tgctagaac tc

22

<210> 119

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 119

1 4 0 / 1 4 3

ctttcagcac gtcaaggaca t

21

<210> 120

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 120

acacctacga aggtacacat gac

23

<210> 121

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 121

gctatttcag ggtaaattgga gtc

23

1 4 1 / 1 4 3

<210> 122

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 122

cagagatgga ggatgtcaat aac

23

<210> 123

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 123

catagcagct ttaaagagac acg

23

<210> 124

1 4 2 / 1 4 3

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 124

ccaccataac agtggagtgg g

21

<210> 125

<211> 24

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 125

cagttacagg tgtatgactg ggag

24

<210> 126

<211> 23

<212> DNA

1 4 3 / 1 4 3

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 126

ctgaatacaa cttcctgttt gcc

23

<210> 127

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 127

gaccacagaa ttacaaaac tgc

23